

RAW SEQUENCE LISTING DATE: 04/19/2001
PATENT APPLICATION: US/09/435,274A TIME: 14:24:55

Input Set : A:\Cpg.pto
Output Set: N:\CRF3\04192001\1435274A.raw

3 <110> APPLICANT: Citovsky, Vitaly H
 4 Rhee, Yoon
 6 <120> TITLE OF INVENTION: Genetic Assay for Protein Nuclear Transport
 8 <130> FILE REFERENCE: 001.00301
 10 <140> CURRENT APPLICATION NUMBER: US 09/435,274A
 11 <141> CURRENT FILING DATE: 1999-11-05
 13 <150> PRIOR APPLICATION NUMBER: US 60/107,417
 14 <151> PRIOR FILING DATE: 1998-11-06
 16 <160> NUMBER OF SEQ ID NOS: 13
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 611
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Unknown Organism
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: Description of Unknown Organism:bacterial
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: modified bacterial lexA
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 33 cagacaggta tgccggccgac gcggtcgaa atcgccgcgc gtttggggtt cgtttcccaa 120
 34 acggggctga ayaacatctg aaggcgctgg caagccaaagg cgttattgaa attgtttccg 180
 35 gcgatcacg cgggattcgt ctgttgcagg aagagganaga aggggttgcgc ctggtaggtc 240
 36 ytgtggctgc cgggtgaacca ctctgtgcgc aacaguatat tgaayglicat talcaggbcg 300
 37 atcccttcctt attcaagccg aatgtgttatt tcctgtgtcg cgtcajcgccc atytcgatga 360
 38 aagatatcgj cattatggat ggtgacttgc tggcagtgc aaaaactcag gatgtacgta 420
 39 acggtcaggjt cgttgcgcg cgtattgtatc aacaaaggatc cgttaaggcc ctggaaaaaac 480
 40 agggcaataa aqtcgaaactg ttgcacaaaa atagcgatgt taaaccattt gtcgttgacc 540
 41 ttctgtcagca gagcttcacc attgaagggc tggcggttgg gtttattcgc aacggcgact 600
 42 ggcttggatt c 611
 45 <210> SEQ ID NO: 2
 46 <211> LENGTH: 204
 47 <212> TYPE: PRT
 48 <213> ORGANISM: Unknown Organism
 50 <220> FEATURE:
 51 <223> OTHER INFORMATION: Description of Unknown Organism:bacterial
 53 <220> FEATURE:
 54 <223> OTHER INFORMATION: modified bacterial lexA
 56 <400> SEQUENCE: 2
 57 Met Lys Ala Leu Thr Ala Arg Gln Gln Glu Val Phe Asp Leu Ile Arg
 58 1 5 10 15
 60 Asp His Ile Ser Gln Thr Gly Met Pro Pro Thr Arg Ala Glu Ile Ala
 61 20 25 30
 63 Gln Arg Leu Gly Phe Arg Ser Pro Asn Ala Ala Glu Glu His Leu Lys
 64 35 40 45
 66 Ala Leu Ala Arg Lys Gly Val Ile Glu Ile Val Ser Gly Ala Ser Arg
 67 50 55 60

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69 Gly Ile Arg Leu Leu Gln Glu Glu Glu Gly Leu Pro Leu Val Gly
 70 65 70 75 80
 72 Arg Val Ala Ala Gly Glu Pro Leu Leu Ala Cln Gln His Ile Glu Gly
 73 85 90 95
 75 His Tyr Gln Val Asp Pro Ser Leu Phe Lys Pro Asn Ala Asp Phe Leu
 76 100 105 110
 78 Leu Arg Val Ser Gly Met Ser Met Lys Asp Ile Gly Ile Met Asp Gly
 79 115 120 125
 81 Asp Leu Leu Ala Val His Lys Thr Cln Asp Val Arg Asn Gly Gln Val
 82 130 135 140
 84 Val Val Ala Arg Ile Asp Asp Glu Val Thr Val Lys Gly Leu Glu Lys
 85 145 150 155 160
 87 Gln Gly Asn Lys Val Glu Leu Leu Pro Glu Asn Ser Glu Phe Lys Pro
 88 165 170 175
 90 Ile Val Val Asp Leu Arg Gln Gln Ser Phe Thr Ile Glu Gly Leu Ala
 91 180 185 190
 93 Val Gly Val Ile Arg Asn Gly Asp Trp Leu Glu Phe
 94 195 200
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 98 <211> LENGTH: 7
 99 <212> TYPE: PRT
 100 <213> ORGANISM: Simian virus 40
 102 <220> FEATURE:
 103 <223> OTHER INFORMATION: Large T antigen NLS
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 106 Pro Lys Lys Lys Arg Lys Val
 107 1 5
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 111 <211> LENGTH: 17
 112 <212> TYPE: PRT
 113 <213> ORGANISM: Xenopus sp.
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 118 <220> FEATURE:
 119 <221> NAME/KEY: VARIANT
 120 <222> LOCATION: (3)..(13)
 121 <223> OTHER INFORMATION: Residues 3 to 13 in Xenopus laevis are Pro Ala Ala
 122 <223> OTHER INFORMATION: Thr Lys Lys Ala Gly Gln Ala Lys
 124 <400> SEQUENCE: 4
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 126 1 5 10 15
 128 Leu
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 133 <211> LENGTH: 9
 134 <212> TYPE: PRT
 135 <213> ORGANISM: Human immunodeficiency virus type 1
 137 <220> FEATURE:
 138 <223> OTHER INFORMATION: Rev protein NES
 140 <400> SEQUENCE: 5

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142 1 5
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146 <211> LENGTH: 9
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150 <220> FEATURE:
151 <223> OTHER INFORMATION: Description of Artificial Sequence:nuclear export
152 signal
154 <220> FEATURE:
155 <223> OTHER INFORMATION: mutated NES of pNEAM10
157 <400> SEQUENCE: 6
158 Leu Pro Pro Asp Leu Arg Leu Thr Leu
159 1 5
162 <210> SEQ ID NO: 7
163 <211> LENGTH: 4
164 <212> TYPE: PRT
165 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: Description of Artificial Sequence:nuclear export
169 signal
171 <220> FEATURE:
172 <223> OTHER INFORMATION: residual NES of pNEARev(delta)3
174 <400> SEQUENCE: 7
175 Leu Pro Pro Leu
176 1
179 <210> SEQ ID NO: 8
180 <211> LENGTH: 26
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Description of Artificial Sequence:primer sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: GAL4 primer
190 <400> SEQUENCE: 8
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195 <211> LENGTH: 27
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Description of Artificial Sequence:primer sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: GAL4 primer
205 <400> SEQUENCE: 9
206 gacggatccc cgggtattcg atctctt 27
209 <210> SEQ ID NO: 10
210 <211> LENGTH: 29
211 <212> TYPE: DNA

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212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
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218 <223> OTHER INFORMATION: GAL4 primer
220 <400> SEQUENCE: 10
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224 <210> SEQ ID NO: 11
225 <211> LENGTH: 27
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Description of Artificial Sequence:primer sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: GAL4 primer
235 <400> SEQUENCE: 11
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240 <211> LENGTH: 25
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247 <220> FEATURE:
248 <223> OTHER INFORMATION: mutant lexA primer
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254 <210> SEQ ID NO: 13
255 <211> LENGTH: 26
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257 <213> ORGANISM: Artificial Sequence
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260 <223> OTHER INFORMATION: Description of Artificial Sequence:primer sequence
262 <220> FEATURE:
263 <223> OTHER INFORMATION: selection lexA primer
265 <400> SEQUENCE: 13
266 gtgactggtg aggccctcaac caagtc 26

VERIFICATION SUMMARY

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L:125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# :4